

ATGACCGCTATGAGCACTGCAATTACACGCCAGATCGTTCTCGATACCGAAACCACCGGTATGAACCAAGATTGGT 75

M T A M S T A I T R Q I V L D T E T T G M N O I G  
\_\_\_\_\_mutD\_\_\_\_\_

GGCAGACTATGAAGGCCACAAGATCATTGAGATTGGTGCCTGTTGAAGTGGTGAACCGGTGCCTGACGGGCAATAAC 150

A H Y E G H K I I E I G A V E V V N R R L T G N N  
\_\_\_\_\_mutD\_\_\_\_\_

TTCCATGTTTATCTCAAACCGGATGGCTGGTGGATCCGGTACATGGTATTGCCGATGAATTI 225

F H V Y L K P D R L V D P E A F G V H G I A D E F  
\_\_\_\_\_mutD\_\_\_\_\_

TTGCTCGATAAGCCCACGTTGCCGAAGTAGCCGATGAGTTCATGGACTATATTGCCGGAGTTGGTGTGATC 300

L E D K P T F A E V A D E F M D Y I R G A E L V I  
\_\_\_\_\_mutD\_\_\_\_\_

CATAACCGAGCGTTCGATATGGACTACGAGTTTCGTTAAGCGCGATATTCCGAAGACCAAT 375

H N A A F D I G F M D Y E F S L L K R D I P K T N  
\_\_\_\_\_mutD\_\_\_\_\_

**FIG.\_1A**

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ACTTTCTGTAAGGTCAACCGATAAGCCTTGGGTGGCGAGGAAAATGTTTCCCGTAAGGGCAACAGCCTCGATGCG 450

mutD

T F C K V T D S L A V A R K M F P G K R N S L D A

TTATGTCGCTACGAAATAGATAACAGTAAACCGAACGCTGCACGGGGCATTACTCGATGCCAGATCCTTGC 525

mutD

L C A R Y E I D N S K R T L H G A L L D A Q I L A

GAAGTTTATCTGGCGATGACCGGGTCAAACGTCGATGGCTTTGCGATGGAAGGGAGAGACACAACAGCAACAA 600

mutD

E V Y L A M T G G O T S M A F A M E G E T Q Q Q Q

GGTGAAGCAACAAATTCAAGCCGATTGTACGTCAAGGCAAGTAAGTTACGGCTTGCGTGTGTTTGGCACAGATGAAAGAGATT 675

mutD

G E A T I Q R I V R Q A S K L R V V F A T D E E I

GCAGGCTCATGAAGCCCGTCTCGATCTGGTGCAGAAGAAAGGGGAAGTTGCCCTCTGGCGAGCATAA 741

mutD

A A H E A R L D L V Q K K G G S C L W R A .

**FIG.-1B**

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10	ATGAGCTATCGTATCTGATTATCTGGTCCAAATGTTGAACTTCTTGGCCGGGGCCC	Eb_429T.dna
10	ATGAGCTATCGTATCTGATTATCTGGTCCAAATGTTGAACTTCTTGGCCGGGGCCC	Eb_GEBT.dna
70	GTTCCTGTTGCTGGCCAGCCGCTGCCAGCTGGCTGGGGGTAAAGCCCTGGTGACCC	Eb_429T.dna
70	GTTCCTGTTGCTGGCCAGCCGCTGCCAGCTGGCTGGGGGTAAAGCCCTGGTGACCC	Eb_GEBT.dna
130	GATAAGGGCTGGCCATTAAAGACGGTGGCTGGATCAGACCGGTGAAGCACCTGAAA	Eb_429T.dna
130	GATAAGGGCTGGCCATTAAAGACGGTGGCTGGATCAGACCGGTGAAGCACCTGAAA	Eb_GEBT.dna
190	GCGGCCGGTATTGAGGTATTGAGGTATTGAGGTATTGAGGTATTGAGGTATTGAGGT	Eb_429T.dna
190	GCGGCCGGTATTGAGGTATTGAGGTATTGAGGTATTGAGGTATTGAGGTATTGAGGT	Eb_GEBT.dna
250	GTCCTGGACGGCCATTGCTGGCCATGTTCCGTAAAGAGGCACTGATAATCACCGTCGGC	Eb_429T.dna
250	GTCCTGGACGGCCATTGCTGGCCATGTTCCGTAAAGAGGCACTGATAATCACCGTCGGC	Eb_GEBT.dna

FIG..2A

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310	GGGGCAGGCCGGCA	CGACTGGTAAAGGCATTGGTATTGGCAGCCACCCGGGTGAT	Eb_429T.dna
310	GGGGCAGGCCGGT	CGACTGGTAAAGGCATTGGTATTGGCAGCCACCCGGGTGAT	Eb_GEBT.dna
370	380	390	400
370	CTGTACAGCTATGCCCGTATCGAAACACTCACCAACCCGCTGCGCCATTGGGGTC	Eb_429T.dna	
370	CTGTACAGCTATGCCCGTATCGAAACACTCACCAACCCGCTGCGCCATTGGGGTC	Eb_GEBT.dna	
430	440	450	460
430	AACACCACCGGGACCCGGAAGTCACCCGCCACTGGCTGACTAACACCAAA	Eb_429T.dna	
430	AACACCACCGGGACCCGGAAGTCACCCGCCACTGGCTGACTAACACCAAA	Eb_GEBT.dna	
490	500	510	520
490	ACCAAGTAAATTGTGATTGTCAAGCTGGCCAACCTGGCTTCCCATTAACGAT	Eb_429T.dna	
490	ACCAAGTAAATTGTGATTGTCAAGCTGGCCAACCTGGCTTCCCATTAACGAT	Eb_GEBT.dna	
550	560	570	580
550	CCGCTGCTGATGATGCCAACGGGGTATGGATGCCCTG	Eb_429T.dna	
550	CCGCTGCTGATGATGCCAACGGGGTATGGATGCCCTG	Eb_GEBT.dna	

FIG.\_2B

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610	ACCCACGGGTAGAGCCCTATCTCCAAAGACGGCAACCCGGTACCGATGCCCTCTGCT	Eb_429T.dna
610	ACCCACGGGTAGAGCCCTATCTCCAAAGACGGCAACCCGGTACCGATGCCCTCTGCT	Eb_GEBT.dna
670	ATTCAAGCCATCAAACCTGATTGCCACCCACTGGCCAGGCCGTCGCCCTGGGACCCAA	Eb_429T.dna
670	ATTCAAGCCATCAAACCTGATTGCCACCCACTGGCCAGGCCGTCGCCCTGGGACCCAA	Eb_GEBT.dna
730	CTCAAAGCCCCGTGAAACATGGCCCTGGCTCTGGCTGGGATGGCCCTTAAACAAAC	Eb_429T.dna
730	CTCAAAGCCCCGTGAAACATGGCCCTGGCTCTGGCTGGGATGGCCCTTAAACAAAC	Eb_GEBT.dna
790	GCCAAACCTGGGCTATGGCTACGGCATGGCTACAGCTGGGCTGGCTACGACATGGCC	Eb_429T.dna
790	GCCAAACCTGGGCTATGGCTACGGCATGGCTACAGCTGGGCTGGCTACGACATGGCC	Eb_GEBT.dna
850	CACGGGGGTGGCAAACGGGGCTGGCTGGCCATGGCTACCCGCTATAACCTGATGGCC	Eb_429T.dna
850	CACGGGGGTGGCAAACGGGGCTGGCTGGCCATGGCTACCCGCTATAACCTGATGGCC	Eb_GEBT.dna

FIG. 2C

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910	CCGGAAATTTGCCGATATCGCCACCTTATGGGGAAACACCCGGTCTTCCACCC	Eb_429T.dna
910	CCGGAAATTTGCCGATATCGCCACCTTATGGGGAAACACCCGGTCTTCCACCC	Eb_GEBT.dna
970		
970	ATGGACCCAGCCGGCATCGCCGCAATTGCCCTCTCTCTAAAGATGTCGGGATC	Eb_429T.dna
970	ATGGACCCAGCCGGCATCGCCGCAATTGCCCTCTCTCTAAAGATGTCGGGATC	Eb_GEBT.dna
1030		
1030	CCGGACCCCTGGTGAACCTGGGGTAAAGAGGGCCACTCCGTACATGCCAAATG	Eb_429T.dna
1030	CCGGACCCCTGGTGAACCTGGGGTAAAGAGGGCCACTCCGTACATGCCAAATG	Eb_GEBT.dna
1090		
1090	CCCCCTGAAAGACGGCAACGCCCTCTCTAAACCCGGCAAGGGAAACGAAATGCC	Eb_429T.dna
1090	CCCCCTGAAAGACGGCAACGCCCTCTCTAAACCCGGCAAGGGAAACGAAATGCC	Eb_GEBT.dna
1150		
1150	GACATTTCGGCAAGGCCATTCTGA	Eb_429T.dna
1150	GACATTTCGGCAAGGCCATTCTGA	Eb_GEBT.dna

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

FIG.\_2D

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10	MSYRWFDDYLVPNNFPGPAGAVSVVGQRCQLLGGKKALLVT	Eb_429T.dna
10	MSYRWFDDYLVPNNFPGPAGAVSVVGQRCQLLGGKKALLVT	Eb_GEBT.dna
130	DKGLRAIKDGAVIDQTVKHLKAAGIEVVIFDGVBPNPKDTN	Eb_429T.dna
130	DKGLRAIKDGAVIDQTVKHLKAAGIEVVIFDGVBPNPKDTN	Eb_GEBT.dna
130	DKGLRAIKDGAVIDQTVKHLKAAGIEVVIFDGVBPNPKDTN	Eb_GEBT.dna
250	VLDGLAMPRKEQCDMIVITVGGGSPE	Eb_429T.dna
250	VLDGLAMPRKEQCDMIVITVGGGSPL	Eb_GEBT.dna
250	VLDGLAMPRKEQCDMIVITVGGGSPL	Eb_GEBT.dna
370	LYSYAGIETLTNPLPPIIAVNTTAGTASEVTRHCVLNTK	Eb_429T.dna
370	LYSYAGIETLTNPLPPIIAVNTTAGTASEVTRHCVLNTK	Eb_GEBT.dna
370	LYSYAGIETLTNPLPPIIAVNTTAGTASEVTRHCVLNTK	Eb_GEBT.dna
490	TKVKPVIIVSWRNLPSVSINDPLLWICKPAGLTAATGMDAL	Eb_429T.dna
490	TKVKPVIIVSWRNLPSVSINDPLLWICKPAGLTAATGMDAL	Eb_GEBT.dna
490	TKVKPVIIVSWRNLPSVSINDPLLWICKPAGLTAATGMDAL	Eb_GEBT.dna

**FIG.\_3A**

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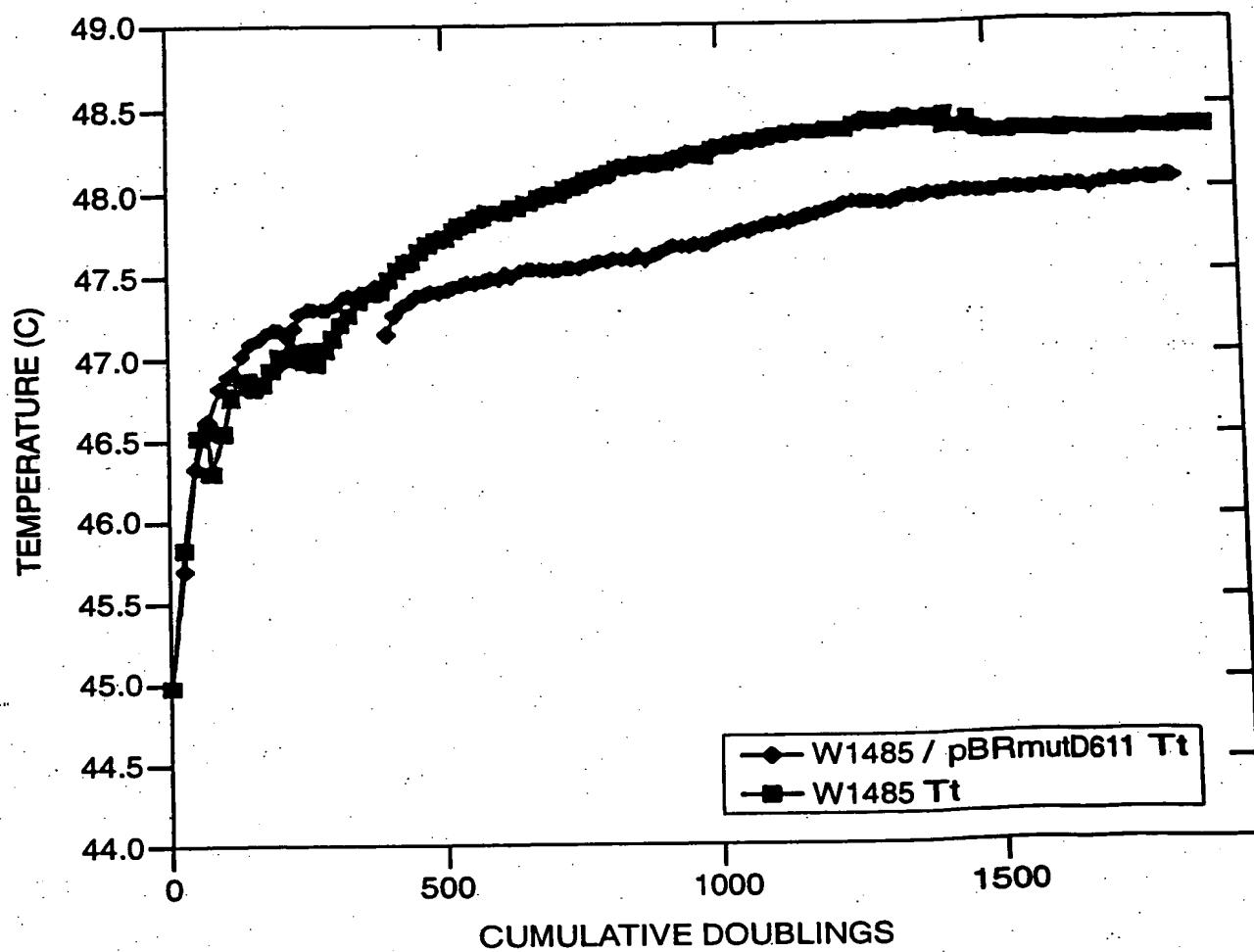
610	THAVEAYISKDANPVTDASAIQAIKLIATNLQAVALGTN	Eb_429T.dna
610	THAVEAYISKDANPVTDASAIQAIKLIATNLQAVALGTN	Eb_GEBT.dna
730	LKARENMACASILLAGMAFNNNANLGYVHAMAHQLGGLYDMA	Eb_429T.dna
730	LKARENMACASILLAGMAFNNNANLGYVHAMAHQLGGLYDMA	Eb_GEBT.dna
850	HGVNAVLLPHVCRYNLLIANPEKPADIATPNCENTTGLST	Eb_429T.dna
850	HGVNAVLLPHVCRYNLLIANPEKPADIATPNCENTTGLST	Eb_GEBT.dna
970	MDAABLAISAIARLSKDVGIPQHLRBLGVKBADFPYMAEM	Eb_429T.dna
970	MDAABLAISAIARLSKDVGIPQHLRBLGVKBADFPYMAEM	Eb_GEBT.dna
1090	ALKDGNAFPSNPRKGNBKBIADIPRQAF	Eb_429T.dna
1090	ALKDGNAFPSNPRKGNBKBIADIPRQAF	Eb_GEBT.dna

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

**FIG.\_3B**



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**FIG.\_4**

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*E. blattae* 33429 pH7  
GLYCEROL FERMENTATION

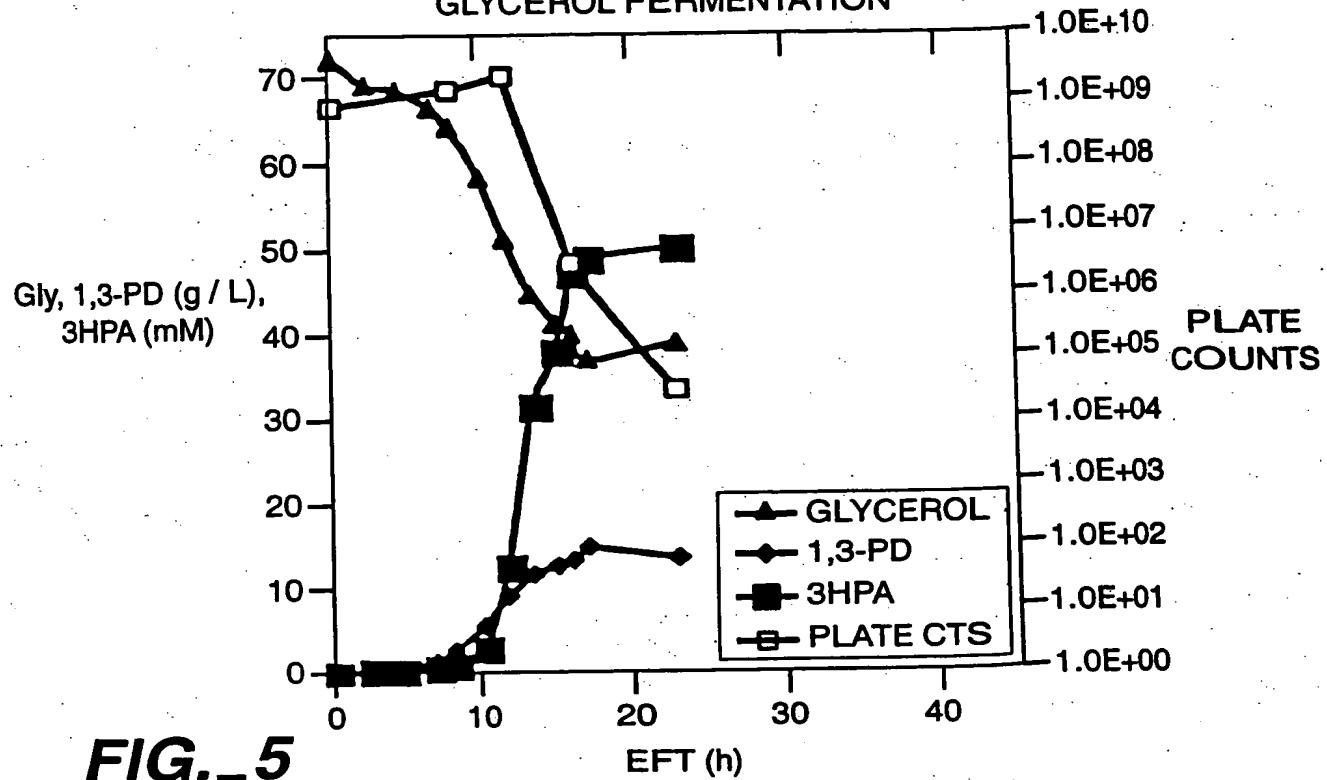


FIG.\_5

*E. blattae* GEB031-4 pH7  
GLYCEROL FERMENTATION

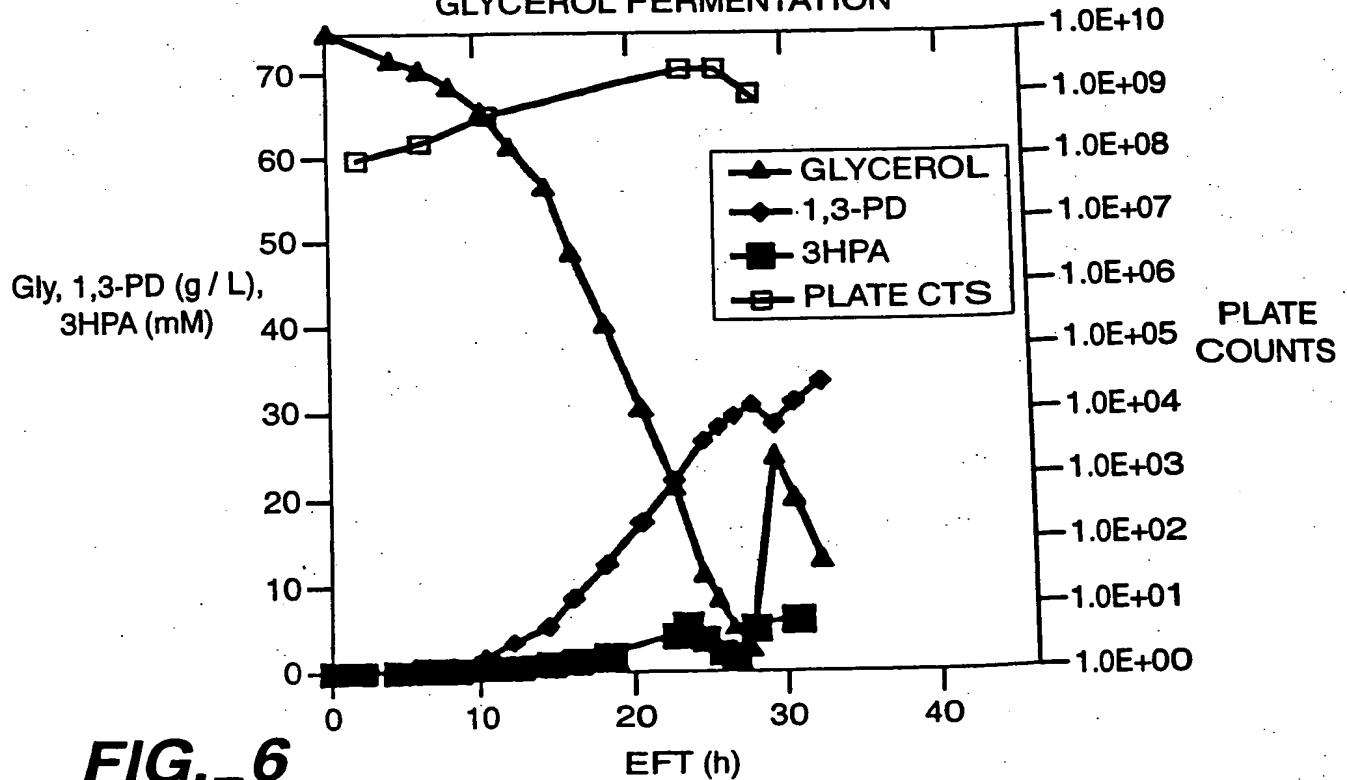


FIG.\_6